Claims

1. A transgenic *Drosophila* whose genome comprises the full-length human colon cancer gene *Adenomatous Polyposis Coli* (APC) having SEQ ID NO.1 wherein:

(a) said genomic alteration allows mis-expression of full-length human APC in flies in regulated manner,

(b) said mis-expression of the full-length human APC results in developmental abnormalities,

(c) said developmental abnormalities induced by the mis-expression of full-length human APC in flies are similar to those exhibited by flies carrying mutations in *Drosophila wingless* gene, and

(d) to use the same as an assay system for screening and validating efficacy of drugs.

2. The transgenic *Drosophila* as claimed in claim 1 wherein, its genome includes β-catenin binding domain comprising of amino-acids from 959 to 1870 of SEQ ID NO. 2 from the full length human APC gene of SEQ ID NO.1, and this engineered disruption of human APC comprises only the five of the seven β-catenin binding domains wherein:

(a) said genomic alteration allows mis-expression of a truncated version of human APC in flies in a regulated manner,

(b) said mis-expression of the said gene construct results in the developmental abnormalities,

(c) said developmental abnormalities induced by the mis-expression of the said gene construct in flies is similar to those exhibited by flies carrying mutations in *Drosophila wingless* gene,

(d) said mis-expression of the said novel construct in regulated manner results in a more severe developmental phenotype, and

(e) to use the same as an assay system for screening and validating efficacy of drugs.

3. The transgenic *Drosophila* as claimed in claim 1 wherein, the N terminal domain of APC with amino acids from 1 to 767 having SEQ ID NO. 3, from the full length human APC gene of SEQ ID NO.1,wherein:

(a) said genomic alteration allows mis-expression of human APC in flies in a regulated manner,

(b) said mis-expression of the said novel construct in a regulated manner resulting in severe abnormalities in fly development during metamorphosis, and

(c) to use the same as an assay system for screening and validating efficacy of drugs.

4. A method for selecting a compound for pharmacological activity, which potentially inhibits or enhances the developmental abnormalities induced by the expression of full length and protein domains of human APC in *Drosophila,* said method comprising:

(a) providing the first, second, and third transgenic fly of claims 1, 2 and 3 respectively, wherein said flies have said developmental abnormalities,

(b) administering the said compounds to the said transgenic *Drosophila* at different concentrations, and

(c) screening for the changes in the severity of the phenotype .

5. A method of determining various *Drosophila* proteins interacting with full-length and protein domains human APC protein wherein, said method comprising:

(a) providing the first, second, and third transgenic fly of claims 1, 2 and 3 respectively, wherein said flies have said developmental abnormalities,

(b) crossing the said transgenic flies individually to a set of *Drosophila* strains each of which carries mutation in a different gene or set of genes, and

(c) Screening for the change in the severity of the phenotype.

6. A method for determining the modulation and differential expression of genes following the mis-expression of full-length and its protein domains human APC in *Drosophila* wherein, said method comprising:

(a) providing the transgenic *Drosophila* as claimed in claims 1,2 and 3 wherein, the flies have developmental abnormalities,

(b) screening for differential gene expression using differential display-RT PCR or microarray techniques, and

(c) identifying genes that are differentially regulated on expression of human APC.

7. A method for determining the modulation and differential expression of proteins following the mis-expression of full-length and its protein domain human APC in *Drosophila* wherein, said method comprising:

(a) providing the transgenic *Drosophila* , as claimed in claims 1, 2 and 3 wherein, the flies have developmental abnormalities,

(b) identifying differential gene expression and protein modifications using proteomics techniques, and

(c) identifying gene products that are differentially regulated on expression of human APC.

8. A method to study Wnt/Wg signaling in *Drosophila* said method comprising;

(a) providing the transgenic *Drosophila*, as claimed in claims 1, 2 and 3,

(b) crossing these transgenic flies to a number of GAL4 drivers to induce targeted expression of said constructs in various tissues and at different developmental stages, and

(c) examining developmental abnormalities.

9. Methods as claimed in claims 6–8 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to study mechanism of various developmental processes such as wing, leg, eye, antennae, and adult cuticle development.

10. A Method as claimed in claim 4 wherein, screening and validating efficacy of preventive and therapeutic drugs following APC gene mis-expression.

11. A Method as claimed in claim 4 wherein, human APC pathway is identified using drug selected from a group of compunds comprising anti inflammatory, Analgesics, Antipyretics, and Antineoplastics.

12. A method as claimed in claim 4 wherein, concentration of said drugs ranging between 50 to 500 μg/ml of fly food.

13. Methods as claimed claims 6-8 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC which has advantages to study the *Drosophila* Wnt/Wg signaling pathway.

14. A Method as claimed in claim 8 wherein, studying the kinetics of Wnt/Wg signaling during various developmental stages and in different tissues.

15. A Method as claimed in claims 5 and 7 wherein, new target proteins interacting with β-catenin are identified.

16. A Method as claimed in claim 6 wherein, genes interacting with APC are identified.

17. Methods as claimed in claims 5–8 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to study biochemical function of human APC function.

18. Methods as claimed in claims 5–8 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to identify additional components of *Drosophila* Wnt/Wg signaling pathway.

19. A transgenic *Drosophila* whose genome comprises the full-length human colon cancer gene *Adenomatous Polyposis Coli* (APC) having SEQ ID NO.1 wherein:

(a) said genomic alteration allows mis-expression of full-length human APC in flies in regulated manner,

(b) said mis-expression of the full-length human APC results in developmental abnormalities,

(c) said developmental abnormalities induced by the mis-expression of full-length human APC in flies are similar to those exhibited by flies carrying mutations in *Drosophila wingless* gene, and

(d) to use the same as an assay system for screening and validating efficacy of anti-cancer drugs.

20. The transgenic *Drosophila* as claimed in claim 19 wherein, its genome includes β-catenin binding domain comprising of amino-acids from 959 to 1870 of SEQ ID NO. 2 from the full length human APC gene of SEQ ID NO.1, and this engineered disruption of human APC comprises only the five of the seven β-catenin binding domains wherein:

(a) said genomic alteration allows mis-expression of a truncated version of human APC in flies in a regulated manner,

(b) the mis-expression of the said gene construct results in the developmental abnormalities,

(c) the developmental abnormalities induced by the mis-expression of the said gene construct in flies is similar to those exhibited by flies carrying mutations in *Drosophila wingless* gene,

(d) mis-expression of the said novel construct in regulated manner results in a more severe developmental phenotype, and

(e) to use the same as an assay system for screening and validating efficacy of anti-cancer drugs.

21. The transgenic *Drosophila* as claimed in claim 19 wherein, the N terminal domain of APC with amino acids from 1 to 767 having SEQ ID NO. 3, from the full length human APC gene of SEQ ID NO.1 wherein:

(a) the said genomic alteration allows mis-expression of human APC in flies in a regulated manner,

(b) the mis-expression of the said novel construct in a regulated manner resulting in severe abnormalities in fly development during metamorphosis, and

(c) to use the same as an assay system for screening and validating efficacy of anti-cancer drugs.

22. A method for selecting a compound for anti-cancer activity, which potentially inhibits or enhances the developmental abnormalities induced by the expression of full length and protein domains of human APC in *Drosophila,* said method comprising:

(a) providing the first, second, and third transgenic fly of claims 19, 20, and 21 respectively, wherein said flies have said developmental abnormalities,

(b) administering the said compounds to the said transgenic *Drosophila* at different concentrations, and

(c) screening for the change in the severity of the phenotype .

23. A method of determining various *Drosophila* proteins interacting with full-length and protein domains human APC protein wherein, said method comprising:

(a) providing the first, second, and third transgenic fly of claims 19, 20, and 21 respectively, wherein said flies have said developmental abnormalities,

(b) crossing the said transgenic flies individually to a set of *Drosophila* strains each of which carries mutation in a different gene or set of genes, and

(c) Screening for the change in the severity of the phenotype.

24. A method for determining the modulation and differential expression of genes following the mis-expression of full-length and its protein domains human APC in *Drosophila* wherein, said method comprising:

(a) providing the transgenic *Drosophila* as claimed in claims 19,20, and 21 wherein, the flies have developmental abnormalities,

(b) screening for differential gene expression using differential display-RT PCR or microarray techniques, and

(c) identifying genes that are differentially regulated on expression of human APC.

25. A method for determining the modulation and differential expression of proteins following the mis-expression of full-length and its protein domain human APC in *Drosophila* wherein, said method comprising:

(a) providing the transgenic *Drosophila* , as claimed in claims 19, 20, and 21 wherein, the flies have developmental abnormalities,

(b) identifying differential gene expression and protein modifications using proteomics techniques, and

(c) identifying gene products that are differentially regulated on expression of human APC.

26. A method to study Wnt/Wg signaling in *Drosophila* said method comprising;

(a) providing the transgenic *Drosophila*, as claimed in claims 19-21,

(b) crossing these transgenic flies to a number of GAL4 drivers to induce targeted expression of said constructs in various tissues and at different developmental stages, and

(c) examining developmental abnormalities.

27. Methods as claimed in claims 24-26 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to study mechanism of various developmental processes such wing, leg, eye, antennae, and adult cuticle development.

28. A Method as claimed in claim 22 wherein, screening and validating efficacy of anti-cancer drugs following APC gene mis-expression.

29. A Method as claimed in claim 22 wherein, human APC pathway is identified using drugs selected from a group of compounds comprising anti inflammatory, Analgesics, Antipyretics, and Antineoplastics.

30. A method as claimed in claim 22 wherein, concentration of said anti-cancer drugs ranging between 50 to 500 μg/ml of fly food.

31. Methods as claimed claims 24-26 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC which has advantages to study the *Drosophila* Wnt/Wg signaling pathway.

32. A Method as claimed in claim 26 wherein, studying the kinetics of Wnt/Wg signaling during various developmental stages and in different tissues.

33. Methods as claimed in claims 23 and 25 wherein, new target proteins interacting with β-catenin are identified.

34. A Method as claimed in claim 24 wherein, genes interacting with APC are identified.

35. Methods as claimed in claims 23-26 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to study biochemical function of human APC function.

36. Methods as claimed in claims 23-26 wherein, examination of developmental abnormalities using gain-of-function genetic model for human APC to identify additional components of *Drosophila* Wnt/Wg signaling pathway.